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Pred. No. is the number of results predicted by chance to have a

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variation in primary sequence and tandem repeat i-antigens of Ichthyophthirius multifillis Mol. Biochem. Parasitol. 120 (1), 93-106 (2002)
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                                                                                                                                                                                                                                                                               /product="immobilization antigen
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/db_xref="G1:12698727"
                                                                                       and
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Lin,Y. Lin,T.-L. and Clark,T.G.
Direct Submission
Submitted (27-NOV-2000) Microbiology an
University, Ithaca, NY 14853, USA
Location/Qualifiers
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                                                                                                                               /organism="Ichthyophthirius
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Ichthyophthirius multifillis.
Eukaryota; Alveolata; Ciliophora; Oligohymenophoraa;
Hymenostomatida; Ophryoglenina; Ichthyophthirius.
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Lin,Y. Lin,T.L., Wang,C.C., Wang,X., Stieger,K., Klopfleisch,R.
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    1520
    /organism "Ichthyophthirius multifiliis"

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Lin.Y., Wang, J.C. and Clark, T.C.
Lin.Y., Wang, J.C. and Clark, T.C.
Direct Submission
Submitted (03-AUG-2001) Microbiology
University, Ithaca, NY 14853, USA
Location/Qualifiers
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                         AGCAACTTATGTCCTGCTGGACTGCAGTTGAAGATGGATCACCTACTTTACTTAATCC 397
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                                                                                                                                                                                                                                                                             The gene for an abundant parasite coat protein predicts tandemly repetitive metal binding domains
                                                                                                                                                                                                                                                                                                                                                     Gaertig,J., Gao,Y., Tishgarten,T., Clark,T.G. and Dickerson,H.W.
Surface display of a parasite antigen in the ciliate Tetrahymena
1358 GCCAGTICCACTITCGCAAAAITITIATCAATGICCTIAATATITATITATITCIATITG 1417
                                                                                               Z486 bp DNA linear INV 19-MA CIACHAYOPHTHIFIUS multifilis immobilization antigen precursor AF140273
                                                                                                                                                                                                            Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Ophryoglenina; Ichthyophthirius.
1 (bases I to 2486)
Clark, T.G., Lin, T.L., Jackwood, D.A., Sherrill, J., Lin, Y. and Dickerson, H.W.
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Clark,T.G., Lin,T.-L., Jackwood,D.A. and Dickerson,H.W.
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/product="immobilization antigen precursor"
/protein_id="AAD31283.1"
/db_xref="GI:4868371"
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/organism="Ichthyophthirius multifiliis"
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Gene 229 (1-2), 91-100 (1999)
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                                         /product="immobilization antigen"
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VPVARGAAAGVAAVTSQCVPCQINKNDSPATRAGQANLATGCSTQCPTGTAIQDGVT
LVFSNSSTQCSQCPTGTATBAHAPGNTATQATQCLTTC
PAGTVLDDGTSTNFVVASATECTKCSAGFFASKTTGFTAATDTTCTECTKKLTSGATAVN
                                                                                                                                                                                                                                               ICYIMANT 118-SEP-1998
IChthyophthirius multifiliis immobilization antigen precursor,
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GNQPFAANNAARGICVPCQINRVGSVTNAGDLATLATQCSTQCPTGTALDDGVTDVFD
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lin, T.L. and Dickerson, H.W.
Purification and partial characterization of immobilization antigens from Ichthyophthirius multifillis
J. Protozool. 39 (4), 457-463 (1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 (bases 1 to 1249)
Clark,T.G., McGraw, R.A. and Dickerson, H.W.
Developmental expression of surface antigen genes in the ciliate Lohthyophthirius multifiliis
Proc. Natl. Acad. Sci. U.S.A. 89 (14), 6363-6367 (1992)
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Ichthyophthirius multifillis
Eukaryota: Alveolata: Ciliophora: Oligohymenophorea;
Hymenostomatida: Ophryoglenina: Ichthyophthirius.
1 (bases 1 to 1249)
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/protein_id="AAC36158.1"
/db_xref="G1:3628569"
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/db_xref="taxon:5932"
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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 46 contigs. The true order of the pieces is not known and their order in this sequence record is
                   Submitted (09-MAY-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases 1 to 175748)
                                                                                                                                             Submitted (23-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA on Jul 18, 2002 this sequence version replaced gi:20514530.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                   Sequencing vector: Plasmid:
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 130722 bases at least Q40
Consensus quality: 143539 bases at least Q20
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*** SEQUENCING IN PROGRESS
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
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Rattus norvegicus clone CH230-22G10,
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180903 bp DNA linear HTG 23-JUL-2002
Rattus norvegicus clone CH230-35H21, *** SEQUENCING IN PROGRESS
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40.1%; Pred. No. 1.1e-07;
Live 0; Mismatches 590; Indels 4
33741 33740: contig of 2667 bp in length 37114: contig of 3274 bp in length 37114: contig of 3274 bp in length 37115: 37214: gap of unknown length 37215: 39781: contig of 2567 bp in length 37318: contig of 2567 bp in length 47719: contig of 3331 bp in length 47719: contig of 3331 bp in length 47719: contig of 3331 bp in length 47749: contig of 3310 bp in length 47749: gap of unknown length 57896: contig of 3407 bp in length 57896: gap of unknown length 57896: gap of unknown length 57896: contig of 3408 bp in length 57897 contig of 3308 bp in length 57896: gap of unknown length 66552: gap of unknown length 72899: gap of unknown length 66553: gap of unknown length 72807: contig of 3308 bp in length 65053: gap of unknown length 66503: gap of unknown length
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Muany, D. M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsorooks, S.L., Amaratunge, H.C., Are, J.R., Agele, M., Banks, T., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Agele, M., Barks, T., Bardow, S.L., Banden, D., Bander, S. B., Blankenburt, R. Bonnin, D., Bouck, J., Border, S. R., Carter, M., Cavazos, S.R., Chacko, J., Chavez, C., Burd, C., Chen, Z., Chowift, T., Christopoulos, C., Carron, T.E., Carter, M., Cavazos, S.R., Chacko, J., Chavez, C., Chen, Z., Chowift, T., Christopoulos, C., Clary, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M. L., Dargar, D., Edwards, C.C., Elhaj, C., Escotto, M., Cavazos, S.R., Charder, C., Davy-Carroll, L., Dederich, D., David, R., Douthwaite, K.J., Drager, H., Dugan Rocha, S., Durbin, H. H., Douthwaite, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Carcia, A., Garcia, A., Laudory, M., Mayua, G., Garcia, A., Laudory, C., Kurceshi, A., Ladouco, R., Laudory, M., Lea, B., Laudory, M., Medua, G., Martin, R., Mar
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Submitted (23-07L-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 117810 bases at least Q40
Consensus quality: 130161 bases at least Q20
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Contact: hgsc-help@bcm.tmc.edu
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COMMENT

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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 69 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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AC022322 186935 bp DNA linear HTG 07-JUL-2000 Homo sapiens chromosome 6 clone RP11-317M22, WORKING DRAFT SEQUENCE, 16 unordered pieces.
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Submitted (30-JAN-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mar 24, 2000 this sequence version replaced g1:7109575.
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                                                                                                                                                                                                                                                                                             arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                  NOTE: This is a 'working draft' sequence. It currently consists of 16 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                  Sequencing vector: plasmid; 08
Sequencing vector: plasmid; 08
Chemistry: Dye-primer ET; 100% of reads
Chemistry: Dye-terminator Big Dye; 0% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 181940 bases at least 040
Consensus quality: 183253 bases at least 030
Consensus quality: 183774 bases at least 020
Insert size: 186000; agarose fp
Insert size: 185435; sum-of-contigs
Quality coverage: 6.94 in Q20 bases; sum-of-contigs
Quality coverage: 7.00 in Q20 bases; sum-of-contigs
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135921: contig of 45599 bp in length
136021: gap of unknown length
186935: contig of 50914 bp in length.
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90222: contig of 26487 bp in length
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gap of unknown length
contig of 4924 bp in length
gap of unknown length
contig of 4835 bp in length
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of 3046 bp in length
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of 6093 bp in length
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gap of unknown length
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of 2713 bp in length
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Web site:http://genome.wustl.edu/gsc/index.shtml
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of 1135 bp in l
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/note="assembly_name:Contig11"
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4699. .5833
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           Center project name: H_NH0317M22
                                          Sequencing vector: M13; 100%
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/db_xref="taxon:9606"
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40007 c 40377 g 51585 t 1504 others
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31066. .40841
/note="assembly_name:Contig17"
40942. .52869
/note="assembly_name:Contig18"
52970. .63635
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Pred. No. 1.3e-07;
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90323. .135921
/note="assembly_name:Contig21"
/note="assembly_name:Contig22"
/note="assembly_name:Contig22
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19938 . 24772
/note="assembly_name:Contig15"
24873 . 30965
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/note="assembly_name:Contig13"
            'note="assembly_name:Contig12"
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/note="assembly_name:Contig20
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* NOTE: This is a 'working draft' sequence. It currently consists of 12 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the flhished sequence as soon as it is available and the accession number will be preserved.
                                Center project name: H_NHO786C19
Sequencing vector: M13, 100%
Chemistry: Dye-trainer ET; 100% of reads
Chemistry: Dye-trainer ET; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 175235 bases at least Q40
Consensus quality: 177213 bases at least Q20
Insert size: 198000; agarose-fp
Insert size: 198000; agarose-fp
Insert size: 178453; sum-of-contigs
Quality coverage: 4.48 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4: contig of 7554 bp in length
4: gap of unknown length
9: gap of unknown length
5: contig of 8695 bp in length
5: gap of unknown length
0: contig of 10026 bp in length
0: contig of 3305 bp in length
0: contig of 26030 bp in length
0: gap of unknown length
1: contig of 2618 bp in length
2: contig of 26518 bp in length
3: gap of unknown length
4: contig of 45736 bp in length
6: gap of unknown length
6: gap of unknown length
7: contig of 45746 bp in length
7: contig of 4574 bp in length
7: contig of 2774 bp in length
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/note="assembly_name:Contig10"
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163120. 166938
/note="assembly_name:Contig8
                         -- Project Information
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/db_xref="taxon:9606"
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On Sep 1, 2000 this sequence version replaced disseases
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                                      7830 rGCTGCTGC-----rGCTGCTGCTACTGTTATTACTGCGATTTCTGTTGCTACTGCTGC 7777
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                                                                               TCCTAATTTCAATCCAGGTAATAGTACATGCCTACCTTGCCCAGCAAATAAAGATTATGG 878
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                                                                                                                                                               TGCTGAAGCCACTGCAGGTGGTGCCGCTACTTTAGCCAAATAATGTAATTTTGCATGCCC
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Web site:http://genome.wustl.edu/gsc/index.shtml
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AC024253.4 GI:9959959
HTG: HTGS_PHASE1; HTGS_DRAFT.
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Waterston, R.H.
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                                                                                                                                                                          Length 179553;
                                                                                                                    1108 others
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                                                                                                                                                                          6; DB 2;
4.1e-07;
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Pred. No. 4.1e-07;
0; Mismatches 756;
                 /note="assembly_name:Contig6"
169413 .171639
/note="assembly_name:Contig7"
17140 .179553
/note="assembly_name:Contig9"
5 a 37751 c 36838 g 54991 t 1
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Best Local Similarity 43.33
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131274 bp DNA linear HTG 29-SEP-2001
Rattus norvegicus clone RP31-289D9 strain Brown Norway, WORKING
DRAFT SEQUENCE, 4 unordered pieces.
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Akher, N. Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
Blakesley, Y.R., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,
Dietrich, N.L., Grantle, S., Guan, X., Gupta, J., Haghighi, P.,
Ho, S.-L., Idol, J.R., Karlins, E., Laric, P., Lee-Lin, S.-O.,
McGloskey, J.C., Maduro, V.B., Masiello, C., Masirian, S.D.,
McCloskey, J.C., McDowell, J., Pearson, R., Prasad, A., Shevchenko, Y.,
Stantripop, S., Thomas, J.W., Thomas, P.J., Touchman, J.W.,
Zhang, L.-H. and Green, E.D.
NISC Comparative Sequencing Initiative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                          175693 CTGATG---CTGTGGCTGCTATTATTGTTGCTGCTATTGCTGTTGTTACTGCTGCTA 175749
                                                                                                                           DD 175930 CIGCIGCIGCIGTPATIGCIGCACITCIGTIGFIGCTACTGCIGATITIGCTATITCIG 175989
                                                                                                                                                                                                                                                                                GTGGAGCAACTAATTATGTAATATTATAAACAGAATGTCTAAATTGTGCTGCTAACTTTT 1018
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                                                                                           1019 ATTTTGATGGTAATATTTCTAGGCAGGAAGTAGTAGATGCAAAGCATGTCCAGCAAATA
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Submitted (29-SEP-2001) NIH Intramural Sequen
Grovemont Circle, Gaithersburg, MD 20877, USA
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HTG; HTGS_PHASE1; HTGS_DRAFT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                                      NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TACTGGTACTGCACTTGATGATGGAGTAACTACTGATTATGTTAGATCATTACAGAATG
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Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.990319 Consensus quality: 130033 bases at least Q40 Consensus quality: 130234 bases at least Q40 Consensus quality: 130286 bases at least Q20 Insert size: 127000; agarose-fp Insert size: 127000; agarose-fp Quality coverage: 9.94x in Q20 bases; sum-of-contigs Quality coverage: 9.64x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 131274;
                                                                                                                                                                                                                                                                                                                                          4803: contig of 4803 bp in length
4903: gap of unknown length
33332: contig of 28429 bp'in length
34432: gap of unknown length
74914: contig of 41482 bp in length
75014: gap of unknown length
131274: contig of 56260 bp in length
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44.8%; Pred. No. 9.1e-07;
Live 0; Mismatches 432;
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Ralus, Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Albans, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Albans, C., Amaratunge, H.C., Ase, J.R., Ayele, M., Banks, T., Barbaria, J., Biaqee, R., Blankenburg, K., Bonnin, D., Barbaria, J., Benton, J., Biaqee, K., Blankenburg, K., Bonnin, D., Bouck, J., Benton, J., Biaqee, K., Bornen, B., Brouck, J., Bryant, N. Bryant, N. Carron, T. R., Carter, M., Cavacos, S.R., Chacko, J., Chavez, D., Carron, T. C., Coyle, M.D., Dabhorne, S.R., David, R., Davis, C., Coyle, M.D., Dabhorne, S.R., David, R., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan, Rochas, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garner, P., Garner, P., Garner, P., Hanliton, K., Harris, C., Harris, C., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Homsi, T., Gyack, Huber, J., Huber, J., Hume, J., Joudeh, S., Katovic, J., Kureshi, A., Lady, M., Laiz, M., Mall, M., Laiz, Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulseged, H., Lozado, R.J., Li, Z., Lichtarge, C., Liu, J., Liu, J., Li, Z., Lichtarge, P., Marting, R., Mahneshwari, M., Mapus, P., Marting, R., Marting, M., Mapus, P., Marting, R., Marting, M., Mapus, P., Marting, M., Mapus, P., Marting, R., Marting, M., Mapus, P., Marting, M., Mapus, P., Marting, M., Mapus, P., Marting, R., Marting, R., Marting, M., More, C., Mitchell, T., Mohabbat, K., Morgan, M., Morgan, M., Mitchell, T., Mohabbat, K., Morgan, M., Morgan, M., Mitchell, T., Mohabbat, K., Morgan, M., Marting, S., Miner, Z., Mitchell, T., Morgan, M., Morgan, M., Marting, M., Marti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus norvegicus clone CH230-9811, *** SEQUENCING IN PROGRESS ***,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                           1038 CTAGGCAGGAAGTAGTAGATGCAAAGCATGTCCAGCAAATAAAGTTTTAAGGCGCTGTAGC 1097
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AAGTGCTGCTGGAGTAAATAATTGGGTAGCACAAAACACTGAATGTACTAATTGTGCTCC 797
                                                   798 TAACTTTTACAATAATAGCTCCTAATTTCAATCCAGGTAATAGTACATGCCTACCTTG
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                                                                                                                                                                                                                                                                                                                                                               Submitted (09-WOV-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One apylor Plaza, Houston, TX 77030, USA (Dases I to 176822)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (12-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Jul 11, 2002 this sequence Version replaced gi:18846108.
       Moser, M., Neal, D., Newtson, J., Newtson, N., Nguyen, A., Nguyen, N.,
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Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap, version 0.990329
Consensus quality: 115453 bases at least 030
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Contact: hgsc-help@bcm.tmc.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1098 AACTGCAGGTGGTACTGCTACTTTAATTGCATAATGTGCCCTTGAATGCCCTGCTGGTAC 1157
                                                                                                                                                                                                                                                                                                                        378 ICCTCCAAATTTTAATGCAGGTGCTAGTACATGCACAGCTTGTCCGGTAAACAGAGTTGG 437
                                                                                                                                                                                                                                                                                                                                                                                      438 TGGTGCATTGACTGCTGGTAATGCCGCTACCATAGTCGCATAATGTAACGTCGCATGTCC 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         618 AGGTAAAAGTTAATGCACACCTTGTCCGGCAATTAAACCTGCTAATGTTGCTTAAGCTAC 677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTTAGGTAATGCTACAATAACGGCATAATGTAACGTTGCATGCCCTGATGGTACTAT 737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               798 TAACTITIACAATAATAATGCTCCTAATTTCAATCCAGGTAATAGTACATGCCTACCTTG 857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  738 AAGTGCTGCTGGAGTAAATTGGGTAGCACAAAACACTGAATGTACTAATTGTGCTCC 797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           858 CCCAGCAAATAAAGATTATGGTGCTGAAGCCACTGCAGGTGGTGGCGCTACTTTAGCCAA 917
                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                Score 90.8; DB 2; Length 176822;
Pred. No. 8.6e-07;
0; Mismatches 432; Indels 0;
                                                          19 ap of unknown length
19 contig of 2142 bp in length
19 contig of 2693 bp in length
19 contig of 2693 bp in length
19 ap of unknown length
19 contig of 1700 bp in length
19 contig of 2222 bp in length
20 contig of unknown length
2222 bp in length
                     bp in length
                                                  2864 bp in length
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                                                                                                                                                                                                                                                           Query Match 6.4 Best Local Similarity 44.8 Matches 350; Conservative
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastlen, V., Bloom, T., Boguslavkly, L., Boukhgalter, B., Choepel, Y., Colamarata, J., Campoplano, A., Chang, J., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Govette, M., Graham, L., Grand-Plerre, N., Farolins, S., Gollymore, A., Rarelas, A., Rells, C., Landen, L., Grand-Plerre, N., Karatas, A., Kells, C., Landed, T., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landeld, T., Matchews, C., McCorriby, M., McEwan, P., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McCarthy, M., McEwan, P., McCarthy, M., McEwan, P., McCarthy, M., Wold, D., Major, J., Wayen, C., Norman, C., Retta, R., Rieback, M., Rieb, R., Schauer, S., Schubback, Raymond, C., Retta, R., Rieback, M., Stolauer, S., Schubback, R., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Vohan, Milson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M., Sulle, R., Wolse, M., Subramanian, A., Subramanian, A., Traylio, J., Ye, W.J., Young, G., Shrift, M., Subramanian, A., Subramanian, A., Subramanian, A., Subramanian, A., Subraman, S., Subramer, A., and Zody, M., Lainer, M., Subramanian, A., Subramanian, A., Traylio, J., Ye, W.J., Young, G., Shrift, M., Subramanian, A., Subraman, A., Subramanian, A
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Submitted (02-WAY-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

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Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastlen, V., Bloom, T., Boguslavkly, L., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, S., Grack, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, S., Grock, S., Goyette, M., Margelo, B., Galagan, J., Gardyna, S., Glade, S., Gord, S., Goyette, M., Illev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, I., Marquis, N., Matthews, C., Macdonald, P., Major, J., Marquis, N., Methews, C., Macdonald, P., Major, J., Marquis, N., Methews, C., Macdonald, P., Major, J., Maldrim, J., Meneus, L., Mihowa, T., Mlenga, V., Murphy, T., Naylor, J., Naylor, C., Noth, D., Collyer, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Rayman, C., Retter, R., Phunkhang, P., Pierre, N., Pollara, V., Rayman, J., Rosetti, M., Roy, A., Santcos, R., Schupback, R., Stanan, S., Severy, P., Spencer, B., Stange-Thomann, N., Stolanovic, N. Strauss, N., Subramanian, A., Talalans, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Travers, M., Travers, M., Travers, M., Travers, N., Travers
                                                                                                                                                                                                                                                                                                                                                                      AC119819 261604 bp DNA 11near HTG 06-MAY-2002
Mus musculus clone RP23-107622, WORKING DRAFT SEQUENCE, 67 ordered
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Birren, B., Linton, L., Nusbaum, C. and Lander, E. Mus musculus, clone RP23-107G22
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Mus musculus.
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                                                                                                   Db 174765 TG 174764
1158 TG 1159
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AC119819/c
LOCUS
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KEYWORDS
SOURCE
ORGANISM
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AUTHORS
TITLE
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REFERENCE
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JOURNAL
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COMMENT

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                                                                                                      Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NOTE: This is a 'working draft' sequence. It currently consists of 67 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  provided by the submittor. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will he preserved.
                                                                                                                                                                                    Center project name: L17592
Center clone name: 1076_22
Center clone name: 1076_22
Center clone name: 1076_22
Sequencing vector: Plasmid; n/a: 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 251231 bases at least Q40
Consensus quality: 253857 bases at least Q30
Consensus quality: 253857 bases at least Q30
Consensus quality: 253857 bases at least Q30
Unsert size: 255004; sum-of-contigs
Quality coverage: 8.2 in Q20 bases; sum-of-contigs
Quality coverage: 7.1 in Q20 bases; sum-of-contigs
On May 6, 2002 this sequence version replaced gi:20389360. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                               Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
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15812: contig of 1031 bp in length
15912: gap of 100 bp
16579: contig of 667 bp in length
16679: qap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6521: gap of 100 bp 7622: contig of 1101 bp in length 7722: gap of 100 bp 833: contig of 613 bp in length 8453: gap of 100 bp 8453: gap of 100 bp 9092: contig of 639 bp in length
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12702 13401: contig of 700 bp in length
13402 13501: gap of 100 bp in length
13502 13936: contig of 435 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    accession number will be preserved.
641: contig of 641 bp in length
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1156: contig of 415 bp in length
5: gap of 100 bp
1891: contig of 635 bp in length
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contig of 693 bp in length
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DD 126566 IGCTCCTGCTGCTGCTGCTGCTGCTGCTGTTACCACTGTTCCTCCTGCTGC 126507
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 261604;
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48414 50012: contig of 1599 bp in length
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51412 52878: contig of 1467 bp in length
                                                                                                                                                                                                                                                                                                                                                                                            166: gap of 100 bp 32647: contig of 1381 bp in length 47: gap of 100 bp 33562: contig of 815 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                       662: gap of 100 bp
34659: contig of 997 bp in length
59: gap of 100 bp
35840: contig of 1081 bp in length
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54272: contig of 1294 bp in length
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26778: contig of 974 bp in length
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28007: gap of 100 bp
29190: contig of 1183 bp in length
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30340: contig of 1050 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (18-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Jul 14, 2002 this sequence version replaced 91:20066062.
                                                                                                                                                                                                                                                                        Eukaryota; Métazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus norvegicus clone CH230-123D20, *** SEQUENCING IN PROGRESS ***, 57 unordered pieces.
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Center: Baylor College of Medicine
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NOTE: This is a 'working draft' sequence. It currently consists of 57 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as arbitrary. Gaps between the contigs are represented as This record will be updated with the flinished sequence as soon as it is available and the accession number will be preserved.
                            Chemistry: Dye-terminator Big Dye: 100% of reads Assembly program: Phrap: version 0.990329 Consensus quality: 738549 bases at least 040 Consensus quality: 79579 bases at least 020 consensus quality: 83355 bases at least 020
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CTTGCCCAGCAAATAAAGATTATGGTGCTGAAGCCACTGCAGGTGGTGCCGCTACTTAG 913
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MOSEC, M., Neal, D., Newtson, J., Newtson, N., Mouyen, M., Neal, D., Newtson, J., Newtson, N., Moyen, A., Neytson, N., Newtson, N., Newtson, N., Newtson, N., Newtson, N., Okwonu, G., Oragunye, N., Ovledo, R., Pace, A., Payton, B., Peery, J., Perez, L., Pickens, R., Pickens, P., Pull, L., Oulles, M., Ren, Y., Rives, M., Rojas, A., Rojubokan, I., Rolfe, M., Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shoshtari, N., Sisson, I., Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H., Stone, R., Tansey, J., Taylor, C., Taylor, P., Tamerisa, A., Tamerisa, R., Tang, H., Tansey, J., Taylor, C., Taylor, P., Taelfrod, B., Thomas, N., Thomas, S., Ward-Moore, S., Warten, R., Washington, C., Watlington, S., Walliamson, A., Wleczyk, R., Wooden, S., Watlington, S., Walliamson, A., Wleczyk, R., Wooden, S., Walliamson, A., Wleczyk, R., Wooden, S., Walliamson, D., Walliamson, D., Nelson, D., Nelson, D., Unbublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (10 APR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
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NOTE: This is a "vorking draft' sequence. It currently consists of 8 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (18-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Jul 14, 2002 this sequence version replaced 91:20330656.
Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S.
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Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 14950 bases at least 040
Consensus quality: 80829 bases at least 030
Consensus quality: 84646 bases at least 020
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Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
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contig of 1133 b
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Center clone name: CH230-228G24
..... Summary Statistics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  854 CITGCCCAGCAAATAAAGATTATGGTGCTGAAGCCACTGCAGGTGGTGCTGCCGCTACTTTAG 913
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                                                                                                                                                                                                                                                                                                                                   614 ATCCAGGTAAAAGTTAATGCACACCTTGTCCGGCAATTAAAACCTGCTAATGTTGCTTAAG 673
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bp in length
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Best Local Similarity 45.4
Matches 308; Conservative
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72224
774424
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74070
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RESULT 14 AY016024

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              VRT 01-FEB-2002
                                                                                                   Takifugu rubripas
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Takifugu.
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Submitted (06-DEC-2000) MRC Molecular Haematology Unit, Institute
of Molecular Medicine, John Radcliffe Hospital, Oxford, Oxon OX3
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Takifûgu rubripes alpha globin gene cluster, complete seguence.
Arûl6024
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Hardison,R., Miller,W., Philipsen,S., Tan-Un,K.C., McMorrow,T.,
Frampton,J., Alter,B.P., Frischauf,A.M. and Higgs,D.R.
Comparative genome analysis delimits a chromosomal domain and
identifies key regulatory elements in the alpha globin cluster
Hum. Mol. Genet. 10 (4), 371-382 (2001)
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Hardison,R., Miller,W., Philipsen,S., Tan-Un,K.C., McMorrow,T.,
Frampton,J., Alter,B.P., Frischauf,A.M. and Higgs,D.R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     359 TTAATTTTTATAATGAAAATGCTCCAAATTT---TAATGCAGGTGCTAGTACATGCACAG 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      416 CTTGTCCGGTAAACAGAGTTGGTGGTGCATTGACTGCTGGTAATGCCGGTACCATAGTCG 475
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Best Local Similarity 45.9%; Pred. No. 6.2e-05;
Matches 316; Conservative 0; Mismatches 370; Indels
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8222 c 8431 g 9023 t
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1. .35793
/organism="Takifugu rubripes"
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1. .35793
                                                     AY016024.1 GI:18463974
                                                                                     Takifugu rubripes
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ACO96684.1 GI.15721942
ACO96684.1 GI.15721942
Takifugu rubripes.
Takifugu rubripes
Eukaryota: Metazoa: Chordata; Craniata: Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha: Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Takifugu.
Tetraodontidae; Takifugu.
E 1 (bases I to 84472)
S Akhter,N. Ayele,K. Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Blakesley,R.W., Maduro,G.L., Maduro,V.B., Mastiello,C., Mastifan,S.D.,
McCloskey,J.C., McDowell,J., Pearson,R., Prasad,A., Shevchenko,Y.,
Stantripop,S., Thomas,J.W., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HTG 22-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AC096684 1472 bp DNA 11near HTG 22-SEP-2003
Takifugu rubripes clone 241N7, WORKING DRAFT SEQUENCE, 3 unordered
                                                                                                                                                                                                                                       32562 CTACTAGTGCTGCTACTACTACTAGTGCTACTGCTACTACTACTACTACGGCTACTA 32621
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Center clone name: 21N07
Center clone name: 21N07
Center clone name: 21N07
Center clone name: 21N07
Sequencing vector: plasmid: n/a; 100% of reads
Sequencing vector: plasmid: n/a; 100% of reads
Assembly program: phrap; version 0.990319
Consensus quality: 83639 bases at least Q40
Consensus quality: 838010 bases at least Q30
Consensus quality: 83900 bases at least Q20
Insert size: 890000; pulse-field-gel
Insert size: 84722; sum-of-contigs
Quality coverage: 12.81x in Q20 bases; agarose-fp
Quality coverage: 11.29x in Q20 bases; sum-of-contigs
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536 ATGTTAGATCATTCACAGAATGTGTTAAATGTAGACTTAAACTTTTACTATAATGGTAATA
                                                                                                       ATGGTAATACTCCTTTCAATCCAGGTAAAAGTTAATGCACACCTTGTCCGGCAATTAAAC
                                                                                                                                                   32622 CIGCIGCIACTACTACTACTACGCCTACTACTGCTGCTACTACTACTACTACTGCGGCTGCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center: NIH Intramural Sequencing Center
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Submitted (22-SEP-2001) NIH Intramural Seq
Grovemont Circle, Galthersburg, MD 20877,
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                                                                                                                                                                                                                                                                                                                  TTGCATGCCCTGATGGTACTATAAGTGCT 744
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AC096684
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VERSION
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JOURNAL
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AUTHORS
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SOURCE
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arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Pred. No. 5.2e-05;
0; Mismatches 600; Indels
                                                                                        10947: contig of 10947 bp in length 11047: gap of unknown length 37566: contig of 26519 bp in length 3466; gap of unknown length 84472: contig of 46806 bp in length.
                                                                                                                                                                                   Location/Qualifiers
1. 84472
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/clone="241N7"
/clone_lib="Incyte Genomics"
1. 10947
                                                                                                                                                                                                                                                                                                                                                                                                                    ture 3767. 84472
700t="assembly_fragment"
20846 a 20937 c 21103 g 21384 t
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/note="assembly_fragment
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Local Similarity 42.4%;
hes 441; Conservative
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